

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 18, 2004, 06:12:39 ; Search time 72.5 Seconds
(without alignments)
11658.348 Million cell updates/sec

Title: US-09-938-956-6
Perfect score: 2908
Sequence: 1 atgagacgatccggaacta.....tattcgagcccttgcattga 1632

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 2099954

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description

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1	2881	98.9	543	9	US-09-938-956-7	Sequence 7, Appli
2	2876	98.9	599	9	US-09-887-586A-22	Sequence 22, Appl
3	2876	98.9	599	9	US-09-903-012-22	Sequence 22, Appl
4	2876	98.9	599	10	US-09-900-797-22	Sequence 22, Appl
5	1633.5	56.2	591	9	US-09-887-586A-24	Sequence 24, Appl
6	1633.5	56.2	591	9	US-09-903-012-24	Sequence 24, Appl
7	1633.5	56.2	591	10	US-09-900-797-24	Sequence 24, Appl
8	1553.5	53.4	590	9	US-09-887-586A-54	Sequence 54, Appl
9	1553.5	53.4	590	9	US-09-903-012-54	Sequence 54, Appl
10	1553.5	53.4	590	10	US-09-900-797-54	Sequence 54, Appl
11	1468	50.5	598	9	US-09-887-586A-26	Sequence 26, Appl
12	1468	50.5	598	9	US-09-903-012-26	Sequence 26, Appl
13	1468	50.5	598	10	US-09-900-797-26	Sequence 26, Appl
14	836	28.7	556	9	US-09-887-586A-32	Sequence 32, Appl
15	836	28.7	556	9	US-09-903-012-32	Sequence 32, Appl
16	836	28.7	556	10	US-09-900-797-32	Sequence 32, Appl
17	806.5	27.7	548	9	US-09-887-586A-2	Sequence 2, Appli
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21	804.5	27.7	548	9	US-09-887-586A-12	Sequence 12, Appl
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26	803.5	27.6	548	9	US-09-887-586A-6	Sequence 6, Appli
27	803.5	27.6	548	9	US-09-903-012-6	Sequence 6, Appli
28	803.5	27.6	548	10	US-09-900-797-6	Sequence 6, Appli
29	793.5	27.3	548	9	US-09-887-586A-4	Sequence 4, Appli
30	793.5	27.3	548	9	US-09-903-012-4	Sequence 4, Appli
31	793.5	27.3	548	10	US-09-900-797-4	Sequence 4, Appli
32	792.5	27.3	548	9	US-09-887-586A-10	Sequence 10, Appl
33	792.5	27.3	548	9	US-09-903-012-10	Sequence 10, Appl
34	792.5	27.3	548	10	US-09-900-797-10	Sequence 10, Appl
35	740.5	25.5	567	12	US-10-424-599-186274	Sequence 186274,
36	734	25.2	548	9	US-09-887-586A-52	Sequence 52, Appl
37	734	25.2	548	9	US-09-903-012-52	Sequence 52, Appl
38	734	25.2	548	10	US-09-900-797-52	Sequence 52, Appl
39	715.5	24.6	618	14	US-10-025-145A-65	Sequence 65, Appl
40	714	24.6	628	9	US-09-887-586A-20	Sequence 20, Appl
41	714	24.6	628	9	US-09-903-012-20	Sequence 20, Appl
42	714	24.6	628	10	US-09-900-797-20	Sequence 20, Appl
43	714	24.6	628	13	US-10-041-007-22	Sequence 22, Appl
44	714	24.6	628	14	US-10-025-145A-4	Sequence 4, Appli
45	704.5	24.2	551	15	US-10-411-066-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1
US-09-938-956-7
; Sequence 7, Application US/09938956
; Patent No. US20020142408A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Sigun
; APPLICANT: Dicosimo, Deana J.
; APPLICANT: Koffas, Matheos
; APPLICANT: Odom, J. Martin
; TITLE OF INVENTION: Production of Monoterpene
; FILE REFERENCE: CL1809 US NA
; CURRENT APPLICATION NUMBER: US/09/938,956
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-0
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Mentha spicata
US-09-938-956-7

Alignment Scores:

Pred. No.: 1.67e-260 Length: 543
Score: 2881.00 Matches: 543
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.07% Indels: 0
DB: 9 Gaps: 0

US-09-938-956-6 (1-1632) x US-09-938-956-7 (1-543)

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Db 21 LeuSerAspTyrLysGluAspLysHisValIleArgAlaSerGluLeuValThrLeuVal 40
QY 121 AAGATGGAACTGGAGAAAGAAACGGGATCAAATTCGAACTTGAGTTGATCGATGACTTG 180
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QY 181 CAGAGGATGGGCTGTCCGATCATTTCCAAATAGAGTTCAAAGAAATCTTGCTCTCTATA 240
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QY 241 TATCTCGACCATCACTATTACAAAGAACCTTTTCCAAAGAAAGGAGGATCTCTACTCC 300
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QY 361 GATAGTTTCAAGAACGAGGAGGTGAGTTCAAAGAAAGCCTTAGCGACGACACAGAGGA 420
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QY 421 TTGTTGCAACTGTATGAAGCTTCTCTTCTGTTGACGGAAGCGGAAACCCAGCTCGAGTCA 480
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QY 481 GCGAGGGAATTCGCCACCAAAATTTTGGAGGAAAGTGAACGAGGGTGGTGTGATGGC 540
Db 161 AlaArgGluPheAlaThrLysPheLeuGluGluLysValAsnGluGlyGlyValAspGly 180
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Db 221 LeuGluLeuAlaIleLeuAspLeuAsnIleValGlnAlaGlnPheGlnGluLeuLys 240
QY 721 GAATCCTTCAGGTGGTGAGAAATACTGGGTTTGTGAGAGCTGCCCTTCGCAAGCGAT 780
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RESULT 2

US-09-887-586A-22
; Sequence 22, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 599

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		; ORGANISM: Mentha spicata			
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QY	64	AGTGACTATAAGGAGGACAAACACACGTGATTAGGGCTTCTGAGCTGGTCACCTTTGGTGAAG	123		
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QY	124	ATGGAACCTGGAGAAAGAACCGGATCAAAATTCGACAACTTGAGTTGATCGATGACTTGCAG	183		
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QY	184	AGGATGGGGCTGTCCGATCATTTCCAAAATGAGTTCAAAGAAATCTTGCTCTCTATATAT	243		
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QY	244	CTCGACCATCAGTATTACAAGAACCCCTTTTCCAAAAGAAAGGAGTCTCTACTCCACA	303		
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QY	304	TCTCTTGCAATTTAGGCTCCTCAGAGAACATGGTTTCAAGTCGCACAGAGGATTTCGAT	363		
Db	158	SerLeuAlaPheArgLeuLeuArgGluHisGlyPheGlnValAlaGlnGluValPheAsp	177		
QY	364	AGTTTCAAGAACGAGAGGGTGAGTTCAAAGAAAGCCCTTAGCGACGACACAGAGGATTG	423		
Db	178	SerPheLysAsnGluGluGlyGluPheLysGluSerLeuSerAspAspThrArgGlyLeu	197		
QY	424	TTGCAACTGTATGAAGCTTCTCTTCTGTTGACGGAAGCGCAAAACCCGCTCGAGTCAGCG	483		
Db	198	LeuGlnLeuTyrGluAlaSerPheLeuLeuThrGluGlyGluThrThrLeuGluSerAla	217		
QY	484	AGGGAATTCGCCACCAAAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGATGGCGAC	543		
Db	218	ArgGluPheAlaThrLysPheLeuGluGluLysValAsnGluGlyGlyValAspGlyAsp	237		
QY	544	CTTTTAAACAAGATCGCATATTTCTTTGGACATCCCTCTTCATTTGGAGGATTAAGGCCA	603		
Db	238	LeuLeuThrArgIleAlaTyrSerLeuAspIleProLeuHisTrpArgIleLysArgPro	257		
QY	604	AATGCACCTGTGTGGATCGAATGGTATAGGAAGAGGCCGACATGAATCCAGTAGTGTG	663		
Db	258	AsnAlaProValTrpIleGluTrpTyrArgLysArgProAspMetAsnProValValLeu	277		
QY	664	GAGCTTGCCATACCTCGACTTAAATATTGTTCAAGCACACAATTTCAAGAGAGAGCTCAAAGAA	723		
Db	278	GluLeuAlaIleLeuAspLeuAsnIleValGlnAlaGlnPheGlnGluGluLeuLysGlu	297		
QY	724	TCCTTCAGGTGGTGAGAAATACTGGGTTTGTGAGAAAGCTGCCCTTCGCAAGGGATAGA	783		
Db	298	SerPheArgTrpTrpArgAsnThrGlyPheValGluLysLeuProPheAlaArgAspArg	317		
QY	784	CTGGTGAATGCTACTTTTGGAACTACTGGGATCATCGAGCCACGTCAGCATGCAAGTGCA	843		
Db	318	LeuValGluCysTyrPheTrpAsnThrGlyIleIleGluProArgGlnHisAlaSerAla	337		
QY	844	AGGATAATGATGGGCAAGTCAACGCTCTGATTACGGTGATCGATGATATTTATGATGTC	903		
Db	338	ArgIleMetMetGlyLysValAsnAlaLeuIleThrValIleAspAspIleTyrAspVal	357		
QY	904	TATGGCACCTTAGAAGAACTCGAAACAATTCACTGACCTCATTCGAAGATGGGATATAAAC	963		
Db	358	TyrGlyThrLeuGluGluLeuGluGlnPheThrAspLeuIleArgArgTrpAspIleAsn	377		
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QY	1144	CACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGCGCAGTCGATAAGTGGGCCCTGT	1203		
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QY	1204	ATGTTAACGCACATATTCTTCCGAGTAACAGATTCGTTTCACAAAGGAGACCCGTCGACAGT	1263		
Db	458	MetLeuThrHisIlePhePheArgValThrAspSerPheThrLysGluThrValAspSer	477		
QY	1264	TTGTACAAATACCACGATTTAGTTTCGTTGGTCACTCTTCGTTCTGCGGCTTTCGTGATGAT	1323		
Db	478	LeuTyrLysTyrHisAspLeuValArgTrpSerPheValLeuArgLeuAlaAspAsp	497		
QY	1324	TTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAATCATTTCAGTCTAC	1383		
Db	498	LeuGlyThrSerValGluGluValSerArgGlyAspValProLysSerLeuGlnCysTyr	517		
QY	1384	ATGAGTGACTACAAATGCATCGGAGCGGAGGCGGAGGAGGAGGATTCCTCCATTCCGCAAGAT	1443		
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QY	1444	GAGGTGTGGAAGAAGATGAATCGGAGAGGAGGAGGAGGAGGATTCCTCCATTCCGCAAGAT	1503		
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QY	1504	TTTATAGGATGTGAGTTGATTTAGGAAGGATGGCGCAGTGTGATACCATATGAGAGAT	1563		
Db	558	PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp	577		
QY	1564	GGGCACGGCACACACACCTATTATACATCAACAATGACAGAACCTTATTCGAGCCCC	1623		
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QY	1624	TTTGCA 1629			
Db	598	PheAla 599			
RESULT 3					
US-09-903-012-22					
; Sequence 22, Application US/09903012					
; Patent No. US20020094557A1					
; GENERAL INFORMATION:					
; APPLICANT: Chappell, Joseph					
; APPLICANT: No. US20020094557A11, Joseph P.					
; APPLICANT: Starks, Courtney M.					
; APPLICANT: Manna, Kathleen R.					
; TITLE OF INVENTION: SYNTHASES					
; FILE REFERENCE: 07678-025001					
; CURRENT APPLICATION NUMBER: US/09/903,012					
; CURRENT FILING DATE: 2001-07-11					
; PRIOR APPLICATION NUMBER: 09/398,395					
; PRIOR FILING DATE: 1999-09-17					
; PRIOR APPLICATION NUMBER: 60/100,993					
; PRIOR FILING DATE: 1998-09-18					
; PRIOR APPLICATION NUMBER: 60/130,628					
; PRIOR FILING DATE: 1999-04-22					
; PRIOR APPLICATION NUMBER: 60/150,262					


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; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Mentha spicata
US-09-903-012-22

Alignment Scores:
Pred. No.:      5,12e-260      Length:      599
Score:          2876.00      Matches:      542
Percent Similarity: 100.00%      Conservative: 0
Best local Similarity: 100.00%      Mismatches: 0
Query Match:      98.90%      Indels:      0
DB:                9      Gaps:      0

US-09-938-956-6 (1-1632) x US-09-903-012-22 (1-599)

QY      4 AGACGATCCGGAACACTACAACCCCTTCGTTGGGATGTCAACTTCATCCAAATCGCTTCTC 63
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QY      64 AGTGACTATAAGGAGGACAAACACGTGATTAGGCTTCTGAGCTGGTCACTTTTGGTGAAG 123
Db      78 SerAspTyrLysGluAspLysHisValIleArgAlaSerGluLeuValThrLeuValLys 97

QY      124 ATGGAACCTGGAGAAAGAAACGGATCAAAATTCGACAACTTGAGTTGATCGATGACTTCGAC 183
Db      98 MetGluLeuGluLysGluThrAspGlnIleArgGlnLeuGluLeuIleAspAspLeuGln 117

QY      184 AGGATGGGCTGTCCCGATCATTCCAAATGAGTTCAAAGAAATCTTGCTCTATATAT 243
Db      118 ArgMetGlyLeuSerAspHisPheGlnAsnGluPheLysGluIleLeuSerSerIleTyr 137

QY      244 CTCGACCATCACTATTACAAGAACCCCTTTTCCAAAAGAAAGAGGATCTCTACTCCACA 303
Db      138 LeuAspHisHisTyrTyrLysAsnProPheProLysGluGluArgAspLeuTyrSerThr 157

QY      304 TCTCTTGCAATTAGGCTCCTCAGAGAACATGGTTTCAAGTCGACACAAGAGGTATTTCGAT 363
Db      158 SerLeuAlaPheArgLeuLeuArgGluHisGlyPheGlnValAlaGlnGluValPheAsp 177

QY      364 AGTTTCAAGAACGAGGAGGTGAGTTCAAAGAAAGCCCTTAGCGACGACACAGAGGATTG 423
Db      178 SerPheLysAsnGluGluGlyGluPheLysGluSerLeuSerAspAspThrArgGlyLeu 197

QY      424 TTGCAACTGTATGAAGCTTCCTTTCTGTTACGGAAGCGGAAACACCGCTCGAGTCAGCG 483
Db      198 LeuGlnLeuTyrGluAlaSerPheLeuLeuThrGluGlyGluThrThrLeuGluSerAla 217

QY      484 AGGGAATTCGCCACCAAAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGATGGCGAC 543
Db      218 ArgGluPheAlaThrLysPheLeuGluGluLysValAsnGluGlyGlyValAspGlyAsp 237

QY      544 CTTTAAACAAGATCGCATATTCTTTTGGACATCCCTCTTCATTGGAGGATTAAAGGCCCA 603
Db      238 LeuLeuThrArgIleAlaTyrSerLeuAspIleProLeuHisTrpArgIleLysArgPro 257

QY      604 AATGCACCTGTGTGATCGAATGGTATAGGAAGAGGCCCGACATGAATCCAGTAGTGTG 663
Db      258 AsnAlaProValTrpIleGluTrpTyrArgLysArgProAspMetAsnProValValLeu 277

QY      664 GAGCTTGCCATACCTGACTTAATATTGTTCAAGCACACAATTTCAAGAAGAGCTCAAAGAA 723
Db      278 GluLeuAlaIleLeuAspLeuAsnIleValGlnAlaGlnPheGlnGluLeuLysGlu 297

QY      724 TCCTTCAGGTGGTGGAGAAATACTGGGTTTGTGAGAAAGCTGCCCTTCGCAAGGGATAGA 783
Db      298 SerPheArgTrpTrpArgAsnThrGlyPheValGluLysLeuProPheAlaArgAspArg 317

QY      784 CTGGTGAATGCTACTTTTGGAAATACTGGGATCATCGAGCCACGTCAGCATGCAAGTGCA 843
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Db      318 LeuValGluCysTyrPheTrpAsnThrGlyIleIleGluProArgGlnHisAlaSerAla 337
QY      844 AGGATAATGATGGGCAAAAGTCAACGCTCTGATTACGGTGATCGATGATATTTATGATGTC 903
Db      338 ArgIleMetMetGlyLysValAsnAlaLeuIleThrValIleAspAspIleTyrAspVal 357
QY      904 TATGGCACCTTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGGAAGATGGGATATAAC 963
Db      358 TyrGlyThrLeuGluGluLeuGlnPheThrAspLeuIleArgArgTrpAspIleAsn 377
QY      964 TCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTTCTTGCACTCAACAACTTCGTC 1023
Db      378 SerIleAspGlnLeuProAspTyrMetGlnLeuCysPheLeuAlaLeuAsnAsnPheVal 397
QY      1024 GATGATACATCGTACGATGTTATGAAGGAGAAAGCGTCAACGTTATACCTTACCTGCGG 1083
Db      398 AspAspThrSerTyrAspValMetLysGluLysGlyValAsnValIleProTyrLeuArg 417
QY      1084 CAATCGTGGTGTGATTGCGGATAAGTATATGTTAGGACGCGGTGGTCTACGGCGGG 1143
Db      418 GlnSerTrpValAspLeuAlaAspLysTyrMetValGluAlaArgTrpPheTyrGlyGly 437
QY      1144 CACAAACCAAGTTTGAAGAGTATTTGGAGAACTCATGGCAGTCGATAAGTGGGCCCTGT 1203
Db      438 HisLysProSerLeuGluGluTyrLeuGluAsnSerTrpGlnSerIleSerGlyProCys 457
QY      1204 ATGTTAACGCAATATTTCTCCGAGTAACAGATTCGTTTCAAAAGAGACCGTCGACAGT 1263
Db      458 MetLeuThrHisIlePhePheArgValThrAspSerPheThrLysGluThrValAspSer 477
QY      1264 TTGTACAAATACCAACGATTTAGTTCGTTGGTTCATCCTTCTGCGGCTTGCTGATGAT 1323
Db      478 LeuTyrLysTyrHisAspLeuValArgTrpSerSerPheValLeuArgLeuAlaAspAsp 497
QY      1324 TTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAATCACTTCAGTGCTAC 1383
Db      498 LeuGlyThrSerValGluGluValSerArgGlyAspValProLysSerLeuGlnCysTyr 517
QY      1384 ATGAGTGACTACAATGCAATCGGAGGCGGAGGCGCGGAAAGCACGTCGAAATGGCTGATAGC 1443
Db      518 MetSerAspTyrAsnAlaSerGluAlaGluAlaArgLysHisValLysTrpLeuIleAla 537
QY      1444 GAGGTGTGGAAGAGATGAATGCGGAGAGGGTGTGCAAGGATTCTCCATTTCGCAAGAT 1503
Db      538 GluValTrpLysLysMetAsnAlaGluArgValSerLysAspSerProPheGlyLysAsp 557
QY      1504 TTTATAGGATGTCAGTTGATTTTAGGAAGCATGGCGCAGTTGATGTACCATATATGGAGAT 1563
Db      558 PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp 577
QY      1564 GGGCAGGCGACACAACACCCCTATTATATACATCAACAAATGACCCAGAACCTTATTCGAGCCC 1623
Db      578 GlyHisGlyThrGlnHisProIleIleHisGlnGlnMetThrArgThrLeuPheGluPro 597
QY      1624 TTTGCA 1629
Db      598 PheAla 599

RESULT 4
US-09-900-797-22
; Sequence 22, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
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; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Mentha spicata
US-09-900-797-22

Alignment Scores:
Pred. No.: 5.12e-260 Length: 599
Score: 2876.00 Matches: 542
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.90% Indels: 0
DB: 10 Gaps: 0

US-09-938-956-6 (1-1632) x US-09-900-797-22 (1-599)

QY 4 AGACGATCCGGAACACTACACCCCTTCTCGTTGGATGTCAACTTCATCCCAATCGCTTCTC 63
Db |||||
58 ArgArgSerGlyAsnTyrAsnProSerArgTrpAspValAsnPheIleGlnSerLeuLeu 77
QY 64 ACTGACTATAAGGAGGACAAACACGTCATTAGCGCTTCTGAGCTGGTCACTTTGGTGAAG 123
Db |||||
78 SerAspTyrLysGluAspLysHisValIleArgAlaSerGluLeuValThrLeuValLys 97
QY 124 ATGGAACCTGGAGAAAGAAACGGATCAAAATTCGACAACTTGAGTTGATCGATCGACTTGCAG 183
Db |||||
98 MetGluLeuGluLysGluThrAspGlnIleArgGlnLeuGluLeuIleAspAspLeuGln 117
QY 184 AGGATGGGGCTGTCCGATCATTTCCAAAATGAGTTCAAAGAAATCTTGCTCTATATAT 243
Db |||||
118 ArgMetGlyLeuSerAspHisPheGlnAsnGluPheLysGluIleLeuSerSerIleTyr 137
QY 244 CTCGACCATCACTATTACAAGAACCCCTTTTCCAAAAGAAAGGGATCTCTACTCCACA 303
Db |||||
138 LeuAspHisHisTyrTyrLysAsnPropheProLysGluGluArgAspLeuTyrSerThr 157
QY 304 TCTCTTGCACTTAGGCTCCTCAGAGAACATGGTTTCAAGTCGCACAGAGGTATTCGAT 363
Db |||||
158 SerLeuAlaPheArgLeuLeuArgGluHisGlyPheGlnValAlaGlnGluValPheAsp 177
QY 364 AGTTTCAAGAACGAGGAGGTGAGTTCAAAGAAAGCCTTAGCGACGACACACGAGGATTG 423
Db |||||
178 SerPheLysAsnGluGluGlyGluPheLysGluSerLeuSerAspAspThrArgGlyLeu 197
QY 424 TTGCAACTGTATGAAGCTTCTCTTCTGTTGACGGAGGCGAAACCCACGCTCGAGTCAGCG 483
Db |||||
198 LeuGlnLeuTyrGluAlaSerPheLeuLeuThrGluGlyGluThrThrLeuGluSerAla 217
QY 484 AGGGAATTGCCACCAAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGATGGCGAC 543
Db |||||
218 ArgGluPheAlaThrLysPheLeuGluGluLysValAsnGluGlyGlyValAspGlyAsp 237
QY 544 CTTTAAACAAGAATCGCATATTCTTTGGACATCCCTCTTCATTGGAGGATTAAAGGCCA 603
Db |||||
238 LeuLeuThrArgIleAlaTyrSerLeuAspIleProLeuHisTrpArgIleLysArgPro 257
QY 604 AATGCACCTGTGTGGATCGAATGGTATAGGAAGAGCGCCGACATGAATCCAGTAGTGTG 663
Db |||||
258 AsnAlaProValTrpIleGluTrpTyrArgLysArgProAspMetAsnProValValLeu 277
QY 664 GAGTTGCCATACCTGACTTAAATATTGTTCAAGCAACAATTCAGAAGAGCTCAAAGAA 723
Db |||||
278 GluLeuAlaIleLeuAspLeuAsnIleValGlnAlaGlnPheGlnGluLeuLysGlu 297
QY 724 TCCTTCAGGTGGTGGAGAAATACCTGGGTTTGTGGAAGCTGCCCTTCGCAAGGGATAGA 783
Db |||||
298 SerPheArgTrpTrpArgAsnThrGlyPheValGluLysLeuProPheAlaArgAspArg 317

QY 784 CTGGTGGAAATGCTACTTTTGGAAATACTGGGATCATCGAGCCACGTCAGCATGCAAGTCA 843
Db |||||
318 LeuValGluCysTyrPheTrpAsnThrGlyIleIleGluProArgGlnHisAlaSerAla 337
QY 844 AGGATAATGATGGGCAAGTCAACGCTCTGATTACGGTGATCGATGATATTTATGATGTC 903
Db |||||
338 ArgIleMetMetGlyLysValAsnAlaLeuIleThrValIleAspAspIleTyrAspVal 357
QY 904 TATGCGACCTTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGAAGATGGGATATAAAC 963
Db |||||
358 TyrGlyThrLeuGluGluGlnPheThrAspLeuIleArgArgTrpAspIleAsn 377
QY 964 TCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTCTTGCACCTCAACAACCTCGTC 1023
Db |||||
378 SerIleAspGlnLeuProAspTyrMetGlnLeuCysPheLeuAlaLeuAsnAsnPheVal 397
QY 1024 GATGATACATCGTACGATGTTATGAAGGAGAAAGCGTCAACGTTATACCTACCTCGCGG 1083
Db |||||
398 AspAspThrSerTyrAspValMetLysGluLysGlyValAsnValIleProTyrLeuArg 417
QY 1084 CAATCGTGGGTTGATTTGGCGGATAAGTATATGTTGAGGCACGGTGGTTCTACGGCGGG 1143
Db |||||
418 GlnSerTrpValAspLeuAlaAspLysTyrMetValGluAlaArgTrpPheTyrGlyGly 437
QY 1144 CACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGGCAGTCGATAAGTGGGCCCTGT 1203
Db |||||
438 HisLysProSerLeuGluGluTyrLeuGluAsnSerTrpGlnSerIleSerGlyProCys 457
QY 1204 ATGTTAAACGCACATATTCTCCGAGTAAACAGATTCTGTTTCCAAAAGGAGACCGTCGACAGT 1263
Db |||||
458 MetLeuThrHisIlePhePheArgValThrAspSerPheThrLysGluThrValAspSer 477
QY 1264 TTGTACAAATACCCAGATTAGTTCTGTTGGTTCATCTCTCGTTCTGCGGCTTGCTGATGAT 1323
Db |||||
478 LeuTyrLysTyrHisAspLeuValArgTrpSerSerPheValLeuArgLeuAlaAspAsp 497
QY 1324 TTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTCCGAAATCACCTTCAGTGTCTAC 1383
Db |||||
498 LeuGlyThrSerValGluGluValSerArgGlyAspValProLysSerLeuGlnCysTyr 517
QY 1384 ATGAGTGACTACAATGTCATCGAGGCGGAGGCGGAGGAGGAGTTCCTCCATTCCGCAAGAT 1503
Db |||||
538 GluValTrpLysLysMetAsnAlaGluArgValSerLysAspSerPropheGlyLysAsp 557
QY 1504 TTTATAGGATGTGCAGTTGATTAGGAAGGATGGCGCAGTTGATGATACCATTAATGGAGAT 1563
Db |||||
558 PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp 577
QY 1564 GGGCAGCGCACACAACCCCTATTATACATCAACAATGACCAGAACCTTATTCGAGCCC 1623
Db |||||
578 GlyHisGlyThrGlnHisProIleIleHisGlnGlnMetThrArgThrLeuPheGluPro 597
QY 1624 TTTGCA 1629
Db |||||
598 PheAla 599

RESULT 5

US-09-887-586A-24
; Sequence 24, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A

```
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-887-586A-24

Alignment Scores:
Pred. No.:      1,11e-143      Length:      591
Score:          1633.50        Matches:      305
Percent Similarity: 75.96%      Conservative: 109
Best Local Similarity: 55.96%    Mismatches:   116
Query Match:     56.17%        Indels:       15
DB:              9             Gaps:         7

US-09-938-956-6 (1-1632) x US-09-887-586A-24 (1-591)
QY      4 AGACGATCCGGAACACTACAACCTTCTCGTTGGGATGTCAACTTCATCCAAATCGCTTCTC 63
Db      57 ArgArgThrGlyGlyTyrGlnProThrLeuTyrAspPheSerThrIleGlnLeuPheAsp 76
QY      64 AGTGACTATAAGAGGACAAACACGATGATAGGCTTCTGAGCTGGTCACTTTGGTGAAG 123
Db      77 SerGluTyrLysGluGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY      124 ATGGAACCTGGAGAAAGAAACGGATCAAATTCGCAAACTTGAGTTGATCGATGACTTGCAG 183
Bb      97 MetLeuLeuGlnGluValAspSerIleGlnArgLeuGluLeuIleAspAspLeuArg 116
QY      184 AGGATGGGCTGTCGATCATTTCCAAAATGAGTTCAAAGAAATCTGTCTCTATATAT 243
Db      117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluIleLeuAsnSerLysTyr 136
QY      244 CTCGACCATCACTATTACAAGAACCCCTTTTCCAAAAGAAAGAAAGGATCTCTACTCCACA 303
Db      137 -----TyrThrAsnAsnGluIle-----AspGluSerAspLeuTyrSerThr 150
QY      304 TCTCTTGCAATTTAGCTCCTCAGAGAACATGTTTCAAGTCGCAACAAGAGGTATTCGAT 363
Db      151 AlaLeuArgPheLysLeuLeuArgGlnTyrAspPheSerValSerGlnGluValPheAsp 170
QY      364 AGTTTCAAGAACGAGGAGGT---GAGTTCAAAGAAAGCCTTAGCGACGACACACAGAGGA 420
Db      171 CysPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY      421 TTGTTGCAACTGTATGAAGCTTCTCTTCTGTGACGGAAGGGCGAAACCCACGCTCGAGTCA 480
Db      191 LeuLeuGlnLeuTyrGluAlaSerPheLeuSerAlaGlnGlyGluGluThrLeuHisLeu 210
QY      481 GCGAGGGAATTCGCCACCAAAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGATGGC 540
Db      211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY      541 GAC-----CTTTTAAAGAATCGCATATTTCTTGGACATCCCTCTTCATTGGAGGATT 594
Db      228 AspIleAsnLeuLeuSerSerIleGluArgAlaLeuGluLeuProThrHisTrpArgVal 247
QY      595 AAAAGGCCAAATGCACTGTGTGGATCGAATGGTATAGGAAGAGGCCCGACATGAATCCA 654
Db      248 GlnMetProAsnAlaArgSerPheIleAspAlaTyrLysArgArgProAspMetAsnPro 267
QY      655 GTAGTGTGGAGCTTGCCATACACTCGACTTAATATATGTTCAAGCACAAATTTCAAGAAGAG 714
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QY      715 CTCAAAGAATCCTTCAGGTGGTGGAGAAATACTGGGTTTGTGAGAAAGCTGCCCTTCGCA 774
Db      288 LeuLysGluAlaSerArgTyrTrpAsnSerThrGlyLeuValHisGluLeuPropheVal 307
QY      775 AGGATAGACTGGTGAATGCTACTTTTGGAAATACTGGGATCATCGAGCCACGTCAGCAT 834
Db      308 ArgAspArgIleValGluCysTyrTyrTrpThrThrGlyValValGluArgArgGluHis 327
QY      835 GCAAGTGCACGATAATGATGGGCAAAAGTCAACGCTCTGTATTACGTTGATCGATGATTT 894
Db      328 GlyTyrGluArgIleMetLeuThrLysIleAsnAlaLeuValThrThrIleAspAspVal 347
QY      895 TATGATGTCTATGGCACCTTAGAAGAACTCGAACAATTCACCTGACCTCATTCGAAGATGG 954
Db      348 PheAspIleTyrGlyThrLeuGluGluLeuGlnLeuPheThrThrAlaIleGlnArgTyr 367
QY      955 GATATAAACTCAATCGACCAACTTCCGATTACATGCAACTGTGCTTCTTGCACCTCAAC 1014
Db      368 AspIleGluSerMetLysGlnLeuProProTyrMetGlnIleCysTyrLeuAlaLeuPhe 387
QY      1015 AACTTTCGTGATGATACATCGTACGATGTTATGAAGGAGAAAGCGTCAACGTTATACCC 1074
Db      388 AsnPheValAsnGluMetAlaTyrAspThrLeuArgAspLysGlyPheAsnSerThrPro 407
QY      1075 TACCTGCGGCAATCGTGGTGTGATTGCGCGGATAAGTATATGTTAGACGACGTCGTTTC 1134
Db      408 TyrLeuArgLysAlaTrpValAspLeuValGluSerTyrLeuIleGluAlaLysTrpTyr 427
QY      1135 TACGGCGGGCACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGCGCAGTCGATAAGT 1194
Db      428 TyrMetGlyHisLysProSerLeuGluGluTyrMetLysAsnSerTrpIleSerIleGly 447
QY      1195 GGGCCCTGTATGTTAAACGCACATATTTCTCCGAGTAACAGATTCTGTTCACAAAGGAGACC 1254
Db      448 GlyIleProIleLeuSerHisLeuPhePheArgLeuThrAspSerIleGluGluAsp 467
QY      1255 GTCGACAGTTTGTACAAAATACCACGATTAGTTAGTTGTTGTTGTTCTCTGTTCTCGGGCTT 1314
Db      468 AlaGluSerMetHisLysTyrHisAspIleValArgAlaSerCysThrIleLeuArgLeu 487
QY      1315 GCTGATGATTTGGAAACCTCGGTGGAGAGGTGAGCAGAGGGGATGTGCGGAAATCACTT 1374
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QY      1375 CAGTGCTACATGAGTGACTACATGATCGATCGAGGCGGAGGCGGAGGAGGAGGAGGAGGAG 1434
Db      508 GlnCysTyrMetAsnGluLysAsnAlaSerGluGluGluAlaArgGluHisValArgSer 527
QY      1435 CTGATAGCGGAGGTGTGGAAGAAGATGAATCGGAGAGGGGTGTGGAAGGATTCTCCATTC 1494
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QY      1495 GGCAAAAGATTTTATAGGATGTGCAGTTGATTTAGGAAGGATGGCGCAGTTGATGTAC--- 1551
Db      546 SerLysTyrPheValGlnValSerAlaAsnLeuAlaArgMetAlaGlnTrpIleTyrGln 565
QY      1552 CATAATGGAGATGGGCGACGACACAAACACCCCTATTATACATCAACAATGACCAGAAC 1611
Db      566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
QY      1612 TTATTCGAGCCCTTT 1626
Db      586 LeuPheAspArgTyr 590
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RESULT 6
US-09-903-012-24
; Sequence 24, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-903-012-24

Alignment Scores:
Pred. No.: 1,11e-143 Length: 591
Score: 1633.50 Matches: 305
Percent Similarity: 75.96% Conservative: 109
Best Local Similarity: 55.96% Mismatches: 116
Query Match: 56.17% Indels: 15
DB: 9 Gaps: 7

US-09-938-956-6 (1-1632) x US-09-903-012-24 (1-591)
QY 4 AGACGATCCGGAAACHTACAAACCCCTTCTCGTTGGATGTCAACTTCATCCAAATCGCTTCTC 63
Db 57 ArgArgThrGlyGlyTyrGlnProThrLeuTrpAspPheSerThrIleGlnLeuPheAsp 76
QY 64 AGTGACTATAAGGAGGACAAACACGTCGATTAGGGCTTCTGAGCTGGTCACCTTTGGTGAAG 123
Db 77 SerGluTyrLysGluGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY 124 ATGGAACCTGGAGAAAGAACGGATCAAAATTCGACAACTTGAGTTGATCGATCGACTTGCAG 183
Db 97 MetLeuLeuGlnGluValAspSerIleGlnArgLeuGluLeuIleAspLeuArg 116
QY 184 AGGATGGGGCTGTCCGATCATTTCCAAAATGAGTTCAAAAGAAAGGATCTTCTCTATATAT 243
Db 117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluIleLeuAsnSerLysTyr 136
QY 244 CTCGACCATCACTATTACAGAACCCTTTTCCAAAAGAAAGGATCTTCTACTCCACA 303
Db 137 -----TyrThrAsnAsnGluIle-----AspGluSerAspLeuTyrSerThr 150
QY 304 TCTCTTGCACTTAGGCTCCTCAGAGAACATGGTTTCAAGTCGCACACAGAGTATTCGAT 363
Db 151 AlaLeuArgPheLysLeuLeuArgGlnTyrAspPheSerValSerGlnGluValPheAsp 170
QY 364 AGTTTCAAGAACGAGGAGGT---GAGTTCAAAGAAAGCCTTAGCGACGACACACAGAGGA 420
Db 171 CysPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY 421 TTGTTGCAACTGTATGAAGCTTCCTTTCTGTTGACGGAAGCGGAAACCCACGTCGAGTCA 480
Db 191 LeuLeuGlnLeuTyrGluAlaSerPheLeuSerAlaGlnGlyGluGluThrLeuHisLeu 210
QY 481 GCGAGGGAATTCGCCACCAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGTGATGGC 540
Db 211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY 541 GAC-----CTTTTAAACAAGATCGCATATCTTTTGACATCCCTCTTTCATTCGAGGATT 594
Db 228 AspIleAsnLeuLeuSerSerIleGluArgAlaLeuGluLeuProThrHisTrpArgVal 247
QY 595 AAAAGGCCAAATGCACCTGTGTGATCGAATGGTATAGGAAGGCCCGACATGAATCCA 654
Db 248 GlnMetProAsnAlaArgSerPheIleAspAlaTyrLysArgArgProAspMetAsnPro 267

QY 655 GTAGTGTGGAGCTTGCCATACCTCGACTTAATAATTTTCAAGCACAAATTCAGAAGAG 714
Db 268 ThrValLeuGluLeuAlaLysLeuAspPheAsnMetValGlnAlaGlnPheGlnGlu 287
QY 715 CTCAAAAGAATCCTTCAGGTGGAGAAATACTGGGTTTGTGAGAAAGTCGCCCTTCGCA 774
Db 288 LeuLysGluAlaSerArgTrpTrpAsnSerThrGlyLeuValHisGluLeuProPheVal 307
QY 775 AGGATAGACTGCTGGAATCTACTTTTGGAAATCTGGGATCATCGAGCCACGTCAGCAT 834
Db 308 ArgAspArgIleValGluCysTyrTyrTrpThrGlyValValGluArgGluHis 327
QY 835 GCAAGTGCAAGGATAATGATGGGCAAGTCAACGCTCTGATTACGGTGTATCGATGATATT 894
Db 328 GlyTyrGluArgIleMetLeuThrLysIleAsnAlaLeuValThrThrIleAspVal 347
QY 895 TATGATGTCTATGGCACCTTAGAAGAACTCGAACAATTCACCTGACCTCATTCGAAGATGG 954
Db 348 PheAspIleTyrGlyThrLeuGluGluLeuGlnLeuPheThrThrAlaIleGlnArgTrp 367
QY 955 GATATAAACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTCTTTCGACTCAAC 1014
Db 368 AspIleGluSerMetLysGlnLeuProProTyrMetGlnIleCysTyrLeuAlaLeuPhe 387
QY 1015 AACTTCGTCGATGATACATCGTACGATGTTTATGAAGGAGAAAGGCGTCAACGTTATACCC 1074
Db 388 AsnPheValAsnGluMetAlaTyrAspThrLeuArgAspLysGlyPheAsnSerThrPro 407
QY 1075 TACCTGCGGCAATCGTGGGTTGATTTGGCGGATAAGTATATGTTAGAGGCACGGTGTTC 1134
Db 408 TyrLeuArgLysAlaTrpValAspLeuValGluSerTyrLeuIleGluAlaLysTrpTyr 427
QY 1135 TACGGCGGCACAAACCAAGTTTGAAGAGATATTTCGAGAACTCATGGCAGTCGATAAGT 1194
Db 428 TyrMetGlyHisLysProSerLeuGluGluTyrMetLysAsnSerTrpIleSerIleGly 447
QY 1195 GGGCCCTGTATGTTAACGCACATATTCTTCGAGTAAACAGATTCGTTCACAAAGGAGACC 1254
Db 448 GlyIleProIleLeuSerHisLeuPhePheArgLeuThrAspSerIleGluGluAsp 467
QY 1255 GTCGACAGTTTGTACAAATPACACGATTTAGTTCTGTCGTCATCCTTCGTTCTCGGGCTT 1314
Db 468 AlaGluSerMetHisLysTyrHisAspIleValArgAlaSerCysThrIleLeuArgLeu 487
QY 1315 GCTGATGATTTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTCCGAAATCACTT 1374
Db 488 AlaAspAspMetGlyThrSerLeuAspGluValGluArgGlyAspValProLysSerVal 507
QY 1375 CAGTGCTACATGAGTGACTACAATGTCATCGGAGGCGGAGCGCGGAAGCACGTCGAATGG 1434
Db 508 GlnCysTyrMetAsnGluLysAsnAlaSerGluGluAlaArgGluHisValArgSer 527
QY 1435 CTGATAGCGGAGGTGTGGAAGAAGATGAATGCGGAGAGGGTGTGGAAGGATTCCTCATTC 1494
Db 528 LeuIleAspGlnThrTrpLysMetMetAsnLysGluMetMetThr-----SerSerPhe 545
QY 1495 GGCAAAGATTTTATAGGATGTGCAGTTGATTTAGGAAGGATGGCGAGTTGATGTAC--- 1551
Db 546 SerLysTyrPheValGlnValSerAlaAsnLeuAlaArgMetAlaGlnTrpIleTyrGln 565
QY 1552 CATAATGGAGATGGGCACGCGCACACACACCCCTATTATACATCAACAAATGACCAGAACC 1611
Db 566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
QY 1612 TTATTCGAGCCCTTT 1626
Db 586 LeuPheAspArgTyr 590

RESULT 7
US-09-900-797-24
; Sequence 24, Application US/09900797
; Publication No. US20030087406A1

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; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. US20030087406A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-900-797-24

Alignment Scores:
Pred. No.: 1,11e-143 Length: 591
Score: 1633.50 Matches: 305
Percent Similarity: 75.96% Conservative: 109
Best Local Similarity: 55.96% Mismatches: 116
Query Match: 56.17% Indels: 15
DB: 10 Gaps: 7

US-09-938-956-6 (1-1632) x US-09-900-797-24 (1-591)
QY 4 AGACGATCCGGAACACTACAACCCCTTCCTCGTTGGGATGTCAACTTCATCCCAATCGCTTCTC 63
Db 57 ArgArgThrGlyGlyTyrglnProthrLeuTrpAspPheSerThrIleGlnLeuPheAsp 76
QY 64 AGTGACTATAAGGAGGACAAACACGCTGATTAGGCTTCTGAGCTGCTCACTTTGGTGAAG 123
Db 77 SerGluTyrlsGluGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY 124 ATGGAACCTGGAGAAAGAAACGGATCAAATTCGACAACTTGAGTTGATCGATGACTTGCGAG 183
Db 97 MetLeuGlnGluGluValAspSerIleGlnArgLeuGluLeuIleAspAspLeuArg 116
QY 184 AGGATGGGCTGCTCGGATCATTTCCAAATAGAGTTCAAAGAAATCTTGCTCTATATAT 243
Db 117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluIleLeuAsnSerLysTy 136
QY 244 CTCGACCATCATATTACAAGAACCCCTTTCCAAAGAAAGAAAGGATCTCTACTCCACA 303
Db 137 -----TyrThrAsnAsnGluIle-----AspGluSerAspLeuTy 150
QY 304 TCTCTTGCACTTTAGCTCCTCAGAGAACATGGTTTTCAGTCGACACAGAGGTATTCGAT 363
Db 151 AlaLeuArgPheLysLeuLeuArgGlnTy 170
QY 364 AGTTTCAAGAACGAGGAGGT---GAGTTCAAAGAAAGCCCTTAGCGACGACACAGAGGA 420
Db 171 CysPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY 421 TTGTTGCAACTGTATGAAGCTTCTCTTCTGTTGACGGAAGGCGAACCACGCTCGAGTCA 480
Db 191 LeuLeuGlnLeuTy 210
QY 481 GCGAGGGAATTCGCCACCAAAATTTTGGAGGAAAGTGAACGAGGCTGTTGATGGC 540
Db 211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY 541 GAC-----CTTTTAACAAGAATCGCATATCTTTGGACATCCCTCTTCATTTGGAGGATT 594
Db 228 AspIleAsnLeuLeuSerIleGluArgAlaLeuGluLeuProThrHisTrpArgVal 247
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QY 595 AAAAGGCCAAATGCACCTGTGTGGATCGAATGGTATAGGAAGAGCCCGACATGAATCCA 654
Db 248 GlnMetProAsnAlaArgSerPheIleAspAlaTyrlsArgArgProAspMetAsnPro 267
QY 655 GTAGTGTGGAGCTTCCATACACTCGACTTAAATATTGTTCAAGCACAAATTTCAAGAAGAG 714
Db 268 ThrValLeuGluLeuAlaLysLeuAspPheAsnMetValGlnAlaGlnPheGlnGlnGlu 287
QY 715 CTCAAAGAATCCTTCAGGTGGTGGAGAAATACCTGGGTTTGTGAGAAAGCTGCCCTTCGCA 774
Db 288 LeuLysGluAlaSerArgTrpTrpAsnSerThrGlyLeuValHisGluLeuPropheVal 307
QY 775 AGGATAGACTGGTGAATGCTACTTTTGAATACTGGGATCATCGAGCCACGTCAGCAT 834
Db 308 ArgAspArgIleValGluCysTy 327
QY 835 GCAAGTGCAGGATAAATGATGGGCAAGTCAACGCTCTGATTACGGTGCATGATATT 894
Db 328 GlyTyrgluArgIleMetLeuThrLysIleAsnAlaLeuValThrIleAspAspVal 347
QY 895 TATGATGCTATGGCACCTTAGAAGAACTCGAACTCAATTCAGCTCATTCGAAGATGG 954
Db 348 PheAspIleTyrglyThrLeuGluGluLeuGlnLeuPheThrThrAlaIleGlnArgTrp 367
QY 955 GATATAAACTCAATCGACCAACTTCCCGATTACATCAACTGTGCTTCTTGCACCTCAAC 1014
Db 368 AspIleGluSerMetLysGlnLeuProTy 387
QY 1015 AACTTTCGTCGATACATCGTACGATGTATGAAGGAGAAAGCGCTCAACGTTATATACC 1074
Db 388 AsnPheValAsnGluMetAlaTy 407
QY 1075 TACCTCGCGCAATCGTGGTTGATTGCGGATAAGTATATGTTAGAGGCACGGTGGTTC 1134
Db 408 TyrlsGluArgLysAlaTrpValAspLeuValGluSerTyrlsGluAlaLysTrpTy 427
QY 1135 TACGGCGGCGCACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGSCAGTCGATAAGT 1194
Db 428 TyrlsGluHisLysProSerLeuGluTy 447
QY 1195 GGGCCCTGTATTAAACGCACATATTTCCGAGTAAACAGATTTCGTTCTCGTTCGCGCTT 1254
Db 448 GlyIleProIleLeuSerHisLeuPheArgLeuThrAspSerIleGluGluGluAsp 467
QY 1255 GTCGACAGTTTGTACAAATACCCAGATTAGTTCTGTTGGTTCATCTCTGTTCTCGCGCTT 1314
Db 468 AlaGluSerMetHisLysTy 487
QY 1315 GCTGATGATTTCGGAACCTCGGTGGAGAGCTGAGCAGAGGGGATGTCGCGAAATCACTT 1374
Db 488 AlaAspAspMetGlyThrSerLeuAspGluValGluArgGlyAspValProLysSerVal 507
QY 1375 CAGTGTACATGACTACTACAATGCATCGAGCGGAGCGGCGGAGGATGTCGAGGATTCCTCCATTC 1434
Db 508 GlnCysTy 527
QY 1435 CTGATAGCGGAGGTGTGGAAGAAGATGAATCGCGGAGAGGGTGTGCGAGGATTCCTCCATTC 1494
Db 528 LeuIleAspGlnThrTrpLysMetMetAsnLysGluMetMetThr-----SerSerPhe 545
QY 1495 GGCAAGAATTTTATPAGGATGTGCAGTTGATTAGGAAGGATGGCGCAGTTGATGTAC--- 1551
Db 546 SerLysTy 565
QY 1552 CATAATGAGATGGGCGACGACACCAACACCTATTATATACATCAACAAATGACCAAGAAC 1611
Db 566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
QY 1612 TTATTCGAGCCCTTT 1626
Db 586 LeuPheAspArgTy 590
RESULT 8
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US-09-887-586A-54
; Sequence 54, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-887-586A-54

Alignment Scores:
Pred. No.: 3.43e-136 Length: 590
Score: 1553.50 Matches: 291
Percent Similarity: 72.48% Conservative: 104
Best Local Similarity: 53.39% Mismatches: 141
Query Match: 53.42% Indels: 9
DB: 9 Gaps: 3

US-09-938-956-6 (1-1632) x US-09-887-586A-54 (1-590)

QY	1	ATGACAGCATCCGGAACACTACAAACCTTCTCGTGGGATGTCAACTTCATCCATCGCTT	60
Db	51	IleArgArgSerGlyAspTyrGlnProSerLeuTyrAspPheAsnTyrIleGlnSerLeu	70
QY	61	CTCAGTGACTATAAGGAGGACAAACACGATGATTAGGCTTCTGAGCTGGTCACTTTGGTG	120
Db	71	AsnThrProTyrLysGluGlnArgHisPheAsnArgGlnAlaGluLeuIleMetGlnVal	90
QY	121	AAGATGGAACCTGGAGAAAGAAACGGATCAAATTCGACAACTTGAGTTGATCGATGCTTG	180
Db	91	ArgMetLeuLeuLysValLysMetGluAlaIleGlnGlnLeuGluLeuIleAspAspLeu	110
QY	181	CAGAGGATGGGCTGTCGATCATTTCCAAATAGCTTCAAAGAAATCTTGCTCTCTATA	240
Db	111	GlnTyrLeuGlyLeuSerTyrPhePheGlnAspGluIleLysGlnIleLeuSerSerIle	130
QY	241	TATCTCGACCATCACTATTACAAAGAACCTTTTCCAAAGAAAGAAAGGGATCTCTACTCC	300
Db	131	HisAsnGluProArgTyrPheHisAsn-----AsnAspLeuTyrPhe	144
QY	301	ACATCTCTTGCAATTTAGGCTCCTCAGAGAACATGGTTTCAAGTCGACACAGAGGTATTC	360
Db	145	ThrAlaLeuGlyPheArgIleLeuArgGlnHisGlyPheAsnValSerGluAspValPhe	164
QY	361	GATAGTTTCAAGAACGAGGAG--GGTGAGTTCAAAGAAAGCCTTAGCGACGACACACAGA	417
Db	165	AspCysPheLysIleGluLysCysSerAspPheAsnAlaAsnLeuAlaGlnAspThrLys	184
QY	418	GGATTGTTGCAACTGTATGAAGCTTCTTCTGTGACGGAAGCGGAAACACGCTCGAG	477
Db	185	GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgGluGlyGluAspThrLeuGlu	204
QY	478	TCAGCGAGGGAATTCGCCACCAAAATTTTGGAGGAAAGTGAACGAGGGTGGT-----	531
Db	205	LeuAlaArgArgPheSerThrArgSerLeuArgGluLysPheAspGluGlyGlyAspGlu	224
QY	532	GTTGATGGCGACCTTTTAAACAAGATCGCATATTTCTTGGACATCCCTCTTCATTGGAGG	591

Db	225	IleAspGluAspLeuSerSerTyrPheArgHisSerLeuAspLeuProLeuHisTyrArg	244
QY	592	ATTAAAGGCCAAATGCACCTGTGTGGATCGAATGGTATAGGAAGAGGCCGACATGAAT	651
Db	245	ValGlnGlyLeuGluAlaArgTyrPheLeuAspAlaTyrAlaArgProAspMetAsn	264
QY	652	CCAGTAGTGTGGAGCTTCCCATACTCGACTTAAATATTGTTCAAGCACAAATTTCAAGAA	711
Db	265	ProLeuIlePheLysLeuAlaLysLeuAsnPheAsnIleValGlnAlaThrTyrGlnGlu	284
QY	712	GAGCTCAAAGAATCCTTCAGGTGGTGGAGAAATACTGGGTGTTGTTGAGAAGCTGCCCTTC	771
Db	285	GluLeuLysAspIleSerArgTyrTyrAsnSerSerCysLeuAlaGluLysLeuProPhe	304
QY	772	GCAAGGATAGACTGGTGGATGCTACTTTTGGAAATACTGGGATCATCGAGCCACGTCAG	831
Db	305	ValArgAspArgIleValGluCysPhePheTyrAlaIleAlaPheGluProHisGln	324
QY	832	CATGCAAGTCAAGGATAATGATGGGCAAAAGTCAACGCTCTGATTACGGTGTATCGATGAT	891
Db	325	TyrSerTyrGlnArgLysMetAlaAlaValIleIleThrPheIleThrIleIleAspAsp	344
QY	892	ATTTATGATGCTATGGCACCTTAGAAGAACTCGAACATTAATCACTGACCTCATTCGAAGA	951
Db	345	ValTyrAspValTyrGlyThrIleGluGluLeuGluLeuLeuThrAspMetIleArgArg	364
QY	952	TGGATATAAACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTCTTGCATCTC	1011
Db	365	TrpAspAsnLysSerIleSerGlnLeuProTyrTyrMetGlnValCysTyrLeuAlaLeu	384
QY	1012	AACAACCTTCGTGATGATACATACGATCGTACGATGTTATGAAGAGAAAGCGTCAACGTTATA	1071
Db	385	TyrAsnPheValSerGluArgAlaTyrAspIleLeuLysAspGlnHisPheAsnSerIle	404
QY	1072	CCCTACCTCGGGCAATCGTGGTGTGATTGGCGGATAAGTATATGTTAGAGGCACGGTGG	1131
Db	405	ProTyrLeuGlnArgSerTyrValSerLeuValGluGlyTyrLeuLysGluAlaTyrTrp	424
QY	1132	TTCTACGGCGGGCACAAACCAAGTTTGAAGAGTATTTGGAGAACTCATGGCAGTCGATA	1191
Db	425	TyrTyrAsnGlyTyrLysProSerLeuGluGluTyrLeuAsnAsnAlaLysIleSerIle	444
QY	1192	AGTGGGCCCTGTATGTTAACGCACATATTTCTCCGAGTAACAGATTCGTTCCACAAAGGAG	1251
Db	445	SerAlaProThrIleIleSerGlnLeuTyrPheThrLeuAlaAsnSerIleAspGluThr	464
QY	1252	ACCGTCGACAGTTTGTACAAATACCAACGATTTAGTTCGTTGGTTCATCCTTCGTTCTCGCG	1311
Db	465	AlaIleGluSerLeuTyrGlnTyrHisAsnIleLeuTyrLeuSerGlyThrIleLeuArg	484
QY	1312	CTTGCTGATGATTTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAATCA	1371
Db	485	LeuAlaAspAspLeuGlyThrSerGlnHisGluLeuGluArgGlyAspValProLysAla	504
QY	1372	CTTCAGTGTACATGAGTGAATCAATGCATCGGAGGCGGAGGCGGAGACCGTGAATA	1431
Db	505	IleGlnCysTyrMetAsnAspThrAsnAlaSerGluArgGluAlaValGluHisValLys	524
QY	1432	TGGCTGATAGCGGAGGTGTGGAAGAAGATGAATGCGGAGAGGGTGTGGAAGGATTCCTCA	1491
Db	525	PheLeuIleArgGluAlaTyrLysGluMetAsnThrValThrThrAlaSerAspCysPro	544
QY	1492	TTCCGCAAAAGATTTTATAGGATGTGCGAGTTGATTTAGGAAGGATGGCGCAGTTGATGAT	1551
Db	545	PheThrAspAspLeuValAlaAlaAlaAsnLeuAlaArgAlaAlaGlnPheIleTyr	564
QY	1552	CATAATGGAGATGGGCACGGCACACAACCCCTATTATATCATCAACAATGACCAAGACC	1611
Db	565	LeuAspGlyAspGlyHisGlyValGlnHisSerGluIleHisGlnGlnMetGlyGlyLeu	584
QY	1612	TTATTCGAGCCCTTT 1626	

Db 585 LeuPheGlnProTyr 589

RESULT 9

US-09-903-012-54

; Sequence 54, Application US/09903012

; Patent No. US20020094557A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20020094557A1, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/903,012

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/100,993

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 54

; LENGTH: 590

; TYPE: PRT

; ORGANISM: Salvia officinalis

US-09-903-012-54

Alignment Scores:

Pred. No.:	3,43e-136	Length:	590
Score:	1553.50	Matches:	291
Percent Similarity:	72.48%	Conservative:	104
Best Local Similarity:	53.39%	Mismatches:	141
Query Match:	53.42%	Indels:	9
DB:	9	Gaps:	3

US-09-938-956-6 (1-1632) x US-09-903-012-54 (1-590)

QY 1 ATGAGACGATCGGAAACTACAAACCTTCTCGTGGGATGTCAACTTCATCCATCGCTT 60

Db 51 IleArgSerGlyAspTyrGlnProSerLeuTyrAspPheAsnTyrIleGlnSerLeu 70

QY 61 CTCAGTGACTATAAGGAGGACAAACACGTGATTAGGGCTTCTGAGCTGGTCACTTTGGTG 120

Db 71 AsnThrProTyrLysGluGlnArgHisPheAsnArgGlnAlaGluLeuIleMetGlnVal 90

QY 121 AAGATGGAACCTGAGAAAGAAACGGATCAAAATTCGACAACTTGAGTTGATCGATGACTTG 180

Db 91 ArgMetLeuLysValLysMetGluAlaIleGlnGlnLeuGluLeuIleAspAspLeu 110

QY 181 CAGAGGATGGGCTGTCCGATCATTTCCAAAATGAGTTCAAAGAAATCTTGTCTCTATA 240

Db 111 GlnTyrLeuGlyLeuSerTyrPhePheGlnAspGluIleLysGlnIleLeuSerSerIle 130

QY 241 TATCTCGACCATCACTATTACAAGAACCTTTTCCAAAAGAAAGGGATCTCTACTCC 300

Db 131 HisAsnGluProArgTyrPheHisAsn-----AsnAspLeuTyrPhe 144

QY 301 ACATCTCTTGTAGGCTCCTCAGAGAACATGTTTCAAGTCGCACAAAGAGGTATTC 360

Db 145 ThrAlaLeuGlyPheArgIleLeuArgGlnHisGlyPheAsnValSerGluAspValPhe 164

QY 361 GATAGTTTCAAGAACGAGGAG--GGTGAGTTCAAAGAAAGCCTTAGCGACGACACCCAGA 417

Db 165 AspCysPheLysIleGluLysCysSerAspPheAsnAlaAsnLeuAlaGlnAspThrLys 184

QY 418 GGATTGTTGCAACTGTATGAGCTTCTCTTCTGTTGACGGAAGGCGAAACCACGCTCGAG 477

Db 185 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgGluGlyGluAspThrLeuGlu 204

QY 478 TCAGCGAGGGAATTCGCCACCAATTTTGGAGGAAAAAGTGAACGAGGGTGGT----- 531

Db 205 LeuAlaArgArgPheSerThrArgSerLeuArgGluLysPheAspGluGlyGlyAspGlu 224

QY 532 GTTGATGGCGACCTTTTAAACAAGATCGCATATTCTTTGGACATCCCTCTTTCATTTGGAGG 591

Db 225 IleAspGluAspLeuSerSerTyrIleArgHisSerLeuAspLeuProLeuHisTyrArg 244

QY 592 ATTAAAGGCCAAATGCACCTGTGTGGATCGAATGTTTAAAGTATGTAAGAGCCGACATGAAT 651

Db 245 ValGlnGlyLeuGluAlaArgTyrPheLeuAspAlaTyrAlaArgProAspMetAsn 264

QY 652 CCAGTAGTGTGGAGCTTGGCATACTCGACTTAAATATTGTTCAAGCACAAATTTCAAGAA 711

Db 265 ProLeuIlePheLysLeuAlaLysLeuAsnPheAsnIleValGlnAlaThrTyrGlnGlu 284

QY 712 GAGCTCAAAGAATCCTTCAGGTGGTGGAGAAATACTGGGTTTGTGAGAAGCTGCCCTTC 771

Db 285 GluLeuLysAspIleSerArgTyrTrpAsnSerSerCysLeuAlaGluLysLeuProPhe 304

QY 772 GCAAGGATAGACTGGTGGAAATGCTACTTTTGAATATACTGGGATCATCGAGCCACGTGAG 831

Db 305 ValArgAspArgIleValGluCysPhePheTyrAlaIleAlaPheGluProHisGln 324

QY 832 CATGCAAGTCCAAGGATAATGATGGGCCAAAGTCAACGCTCTGATTACGGTGTATCGATGAT 891

Db 325 TyrSerTyrGlnArgLysMetAlaAlaValIleIleThrPheIleThrIleIleAspAsp 344

QY 892 ATTTATGATGTCTATGGCACCTTTAGAAAGAACTCGAAACAATTCATGACCTCATTCGAAGA 951

Db 345 ValTyrAspValTyrGlyThrIleGluGluLeuGluLeuLeuThrAspMetIleArgArg 364

QY 952 TGGGATATAAACTCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTCTTTCACACTC 1011

Db 365 TrpAspAsnLysSerIleSerGlnLeuProTyrTyrMetGlnValCysTyrLeuAlaLeu 384

QY 1012 AACAACTTCGTGATGATACATCGTACGATGTTTATGAAGGAGAAAGCGTCAACGTTATA 1071

Db 385 TyrAsnPheValSerGluArgAlaTyrAspIleLeuLysAspGlnHisPheAsnSerIle 404

QY 1072 CCCTACCTGCGCAATCGTGGTTGATTGGCGGATAAGTATATGTAGAGGCACGGTGG 1131

Db 405 ProTyrLeuGlnArgSerTyrValSerLeuValGluGlyTyrLeuLysGluAlaTyrTyr 424

QY 1132 TTCTACGGCGGCGACAAACCAAGTTTGGAAAGAGTATTTGGAGAACTCATGGCAGTCGATA 1191

Db 425 TyrTyrAsnGlyTyrLysProSerLeuGluGluTyrLeuAsnAlaLysIleSerIle 444

QY 1192 AGTGGGCCCTGTATGTTAAGCAGCATATTTCTCCGAGTAACAGATTGTTTCAAAAGGAG 1251

Db 445 SerAlaProThrIleIleSerGlnLeuTyrPheThrLeuAlaAsnSerIleAspGluThr 464

QY 1252 ACCGTGACAGTTGTACAAATACCAACGATTTAGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1311

Db 465 AlaIleGluSerLeuTyrGlnTyrHisAsnIleLeuTyrLeuSerGlyThrIleLeuArg 484

QY 1312 CTTGCTGATGATTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTCCGAAATCA 1371

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QY 1372 CTTGAGTGTACATGAGTACATCATCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1431

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Db 525 PheLeuIleArgGluAlaTyrLysGluMetAsnThrValThrThrAlaSerAspCysPro 544

QY 1492 TTCGGCAAAGATTTATAGGATGTGCAGTTGATTTAGGAAGGATGGCGCAGTTGATGTAC 1551

Db 545 PheThrAspAspLeuValAlaAlaAlaAsnLeuAlaArgAlaAlaGlnPheIleTyr 564

QY 1552 CATAATGGAGATGGGCACGCACACACACCCCTATTATACATCAACAAATGACCAGAAC 1611

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Db      565 LeuAspGlyAspGlyHisGlyValGlnHisSerGluIleHisGlnMetGlyGlyLeu 584
      1612 TTATTCGAGCCCTTT 1626
      585 LeuPheGlnProTyr 589

RESULT 10
US-09-900-797-54
; Sequence 54, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-900-797-54

Alignment Scores:
Pred. No.:      3,43e-136      Length:      590
Score:          1553.50      Matches:      291
Percent Similarity: 72.48%      Conservative: 104
Best Local Similarity: 53.39%      Mismatches:  141
Query Match:    53.42%      Indels:       9
DB:             10          Gaps:         3

US-09-938-956-6 (1-1632) x US-09-900-797-54 (1-590)
QY      1  ATGAGACGATCCGGAACTACAAACCTTCTCGTTGGGATGTCAACTTCATCCAACTGCTT 60
      51  IleArgSerGlyAspTyrGlnProSerLeuTyrAspPheAsnTyrIleGlnSerLeu 70
QY      61  CTCAGTACTATAAGGAGGACAAACACGTCGATTAGGCTTCTGAGCTGGTCACTTTGGTG 120
      71  AsnThrProTyrLysGluGlnArgHisPheAsnArgGlnAlaGluLeuIleMetGlnVal 90
QY      121  AAGATGGAACCTGGAGAAAGAAACCGATCAAATTCGACAACTTGAGTTGATCGATGACTTG 180
      91  ArgMetLeuLeuLysValLysMetGluAlaIleGlnGlnLeuGluLeuIleAspAspLeu 110
QY      181  CAGAGGATGGGCTGTCCGATCATTTCCAAATAGATTCAAAGAAATCTTGTCTCTATA 240
      111  GlnTyrLeuGlyLeuSerTyrPhePheGlnAspGluIleLysGlnIleLeuSerSerIle 130
QY      241  TATCTCGACCATCACTATTACAAGAACCTTTTCCAAAGAAAGGATCTCTACTCC 300
      131  HisAsnGluProArgTyrPheHisAsn-----AsnAspLeuTyrPhe 144
QY      301  ACATCTCTTGCAATTAGGCTCCTCAGAGAACATGGTTTTCAGTCCGACAAAGAGGATTC 360
      145  ThrAlaLeuGlyPheArgIleLeuArgGlnHisGlyPheAsnValSerGluAspValPhe 164
QY      361  GATAGTTTCAAGAACGAGGAG---GGTGAGTTCAAAGAAAGCCTTAGCGACGACACACAGA 417
      165  AspCysPheLysIleGluLysCysSerAspPheAsnAlaAsnLeuAlaGlnAspThrLys 184
      418  GGATTGTTGCAACTGTATGAAGCTTCTCTTTCTGTGTGACGGAAGCGGAAACACCGCTCGAG 477
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Db      185 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgGluGlyGluAspThrLeuGlu 204
      478  TCACCGAGGGAATTCGCCCAACCAATTTTGGAGGAAAAAGTGAACGAGGGTGGT----- 531
      205  LeuAlaArgArgPheSerThrArgSerLeuArgGluLysPheAspGluGlyGlyAspGlu 224
      532  GTTGATGGCGACCTTTTAAACAAGAATCGCATATTCTTTGGACATCCCTCTTCTTCTGGAGG 591
      225  IleAspGluAspLeuSerSerTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg 244
      592  ATTAAGAGCCCAATGACCTGTGTGGATCGAATGGTATAGGAAGAGGCCCGACATGAAT 651
      245  ValGlnGlyLeuGluAlaArgTrpPheLeuAspAlaTyrAlaArgArgProAspMetAsn 264
      652  CCAGTAGTGTGGAGCTTGGCATACTCGACTTAAATATTGTTCAAGCACAAATTTCAAGAA 711
      265  ProLeuIlePheLysLeuAlaLysLeuAsnPheAsnIleValGlnAlaThrTyrGlnGlu 284
      712  GAGCTCAAAGAAATCCTTCAGGTGCTGGAGAAATACTGGGTTGTTGAGAAAGCTGCCCTTC 771
      285  GluLeuLysAspIleSerArgTrpTrpAsnSerSerCysLeuAlaGluLysLeuProPhe 304
      772  GCAAGGATAGACTGGTGGAAATGCTACTTTTGGAAATACCTGGGATCATCGAGCCACGTCAG 831
      305  ValArgAspArgIleValGluCysPhePheTrpAlaIleAlaPheGluProHisGln 324
      832  CATGCAAGTCAAGGATAATATGATGGGCAAAAGTCAACGCTCTGATTAACGTTGATCGATGAT 891
      325  TyrSerTyrGlnArgLysMetAlaAlaValIleIleThrPheIleThrIleIleAspAsp 344
      892  ATTTATGATGTCTATGGCACCTTAGAAGAACTCGAACAAATCACTACCTCATTCGAAGA 951
      345  ValTyrAspValTyrGlyThrIleGluGluLeuGluLeuLeuThrAspMetIleArgArg 364
      952  TGGGATATAAACTCAATCGACCACTTCCCGATTACATGCAACTGTGCTTTCTTGCACCTC 1011
      365  TrpAspAsnLysSerIleSerGlnLeuProTyrTyrMetGlnValCysTyrLeuAlaLeu 384
      1012  AACAACTTCGTCGATGATACATCGTACGATGTTATGAAGGAGAAAGCGTCAACGTTATA 1071
      385  TyrAsnPheValSerGluArgAlaTyrAspIleLeuLysAspGlnHisPheAsnSerIle 404
      1072  CCCTACCTGCGGCAATCGTGGTGTGATTGGCGGATAAGTATATAGTAGGACGCGTGG 1131
      405  ProTyrLeuGlnArgSerTrpValSerLeuValGluGlyTyrLeuLysGluAlaTyrTrp 424
      1132  TTCTACGGCGGCGACAAACCAAGTTTGGAAAGAGTATTGGAGAACTCATGGCAGTCGATA 1191
      425  TyrTyrAsnGlyTyrLysProSerLeuGluGluTyrLeuAsnAsnAlaLysIleSerIle 444
      1192  AGTGGGCCCTGTATGTTAAACGCACATATTCTCCGAGTAACAGATTGTTTCAAAAGGAG 1251
      445  SerAlaProThrIleIleSerGlnLeuTyrPheThrLeuAlaAsnSerIleAspGluThr 464
      1252  ACCGTCGACAGTTGTACAAATACCACGATTTAGTTCTGTTGGTTCATCTTCTGCGG 1311
      465  AlaIleGluSerLeuTyrGlnTyrHisAsnIleLeuTyrLeuSerGlyThrIleLeuArg 484
      1312  CTTGCTGATGATTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGGATGTCCCGAAATCA 1371
      485  LeuAlaAspAspLeuGlyThrSerGlnHisGluLeuGluArgGlyAspValProLysAla 504
      1372  CTTCAGTGTACATGAGTGACTACAATGTCATCGAGGCGGAGGCGCGGAGACACGTAATA 1431
      505  IleGlnCysTyrMetAsnAspThrAsnAlaSerGluArgGluAlaValGluHisValLys 524
      1432  TGGCTGATAGCGGAGGTGTGGAAGAGATGAATCGGAGAGGGGTGTCGAAGGATTCTCCA 1491
      525  PheLeuIleArgGluAlaTrpLysGluMetAsnThrValThrThrAlaSerAspCysPro 544
      1492  TTCGGCAAAGATTTATAGGATGTGCACTGTGATTTAGGAAGGATGGCCGAGTTGATGTAC 1551
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173	AsnCysPheLysAsnGlnLysGlyIleAspPheLysAlaSerLeuAlaGlnAspThrLys	192
418	GGATTGTTGCAACTGTATGAAGCTTCTCTTTCTGTTGACGGAAGCGGAAACCCACGCTCGAG	477
193	GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgLysGlyGluAspThrLeuGlu	212
478	TCAGCGAGGGAATTCCGCCACCAAAATTTTGGAGGAAAAGTGAACGAGGGTGGT-----	531
213	LeuAlaArgGluPheAlaThrLysCysLeuGlnLysLysLeuAspGluGlyGlyAsnGlu	232
532	GTTGATGGCGACCTTTTAAACAAGAATCGCATATTCTTTTGGACATCCCTCTTTCATTGGAGG	591
233	IleAspGluAsnLeuLeuLeuTyrPheArgHisSerLeuAspLeuProLeuHisTyrPArg	252
592	ATTTAAAGGCCAAATGCACCTGTGTGGATCGAATGGTATAGGAAGAGGCCCGACATGAAT	651
253	IleGlnSerValGluAlaArgTyrPheIleAspAlaTyrAlaArgArgProAspMetAsn	272
652	CCAGTACTGTTGGAGCTTGCCATFACTCGACTTAAATATTGTTCAAGCACAATTTCAAGAA	711
273	ProLeuIlePheGluLeuAlaLysLeuAsnPheAsnIleIleGlnAlaThrHisGlnGln	292
712	GAGCTCAAGAATCCTTCAGGTGTGGAGAAATACTGGGTTTGTGAGAAGCTGCCCTTC	771
293	GluLeuLysAspLeuSerArgTyrTrpSerArgLeuCysPheProGluLysLeuProPhe	312
772	GCAAGGGATAGACTGGTGGAAATGCTACTTTTGGAAATACTGGGATCATCGAGCCACGTGAT	831
313	ValArgAspArgLeuValGluSerPheTyrPheTrpAlaValGlyMetPheGluProHisGln	332
832	CATGCAAGTCCAAGGATAATGATGGGCAAGTCAACGCTCTGATTACGGTGCATCGATGAT	891
333	HisGlyTyrGlnArgLysMetAlaAlaThrIleIleValLeuAlaThrValIleAspAsp	352
892	ATTTATGATGCTATGGCACCTTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGAAGA	951
353	IleTyrAspValTyrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg	372
952	TGGGATATAAATCAATCGACCAACTTCCCGATTACATGCAACTGTGCTTCTTTCGCACTC	1011
373	TrpAspThrGluSerIleThrArgLeuProTyrTyrMetGlnLeuCysTyrTrpGlyVal	392
1012	AACAACCTTCGTCGATGATACATCGTACGATGTTATGAAGGAGAAAGGCGTCAACGTTATA	1071
393	HisAsnTyrIleSerAspAlaAlaTyrAspIleLeuLysGluHisGlyPhePheCysLeu	412
1072	CCCTACCTCGGGCAATCGTGGTGTGATTTCGCGGATAAGTATATGGTAGAGGCACGGTGG	1131
413	GlnTyrLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTyr	432
1132	TTCTACGGCGGCACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGGCAGTCGATA	1191
433	TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal	452
1192	AGTGGGCGCTGTATGTTAAACGCACATATTCCTCCGAGTAAACAGAT--TCGTTCAAAAG	1248
453	AlaSerProAlaIleIleSerProThrTyrPheThrPheAlaAsnAlaSerHisAspThr	472
1249	GAGACCGTCGACAGTTTGTACAAATACCCAGATTTAGTTTCGTTGGTTCATCCTTCGTTCTG	1308
473	AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu	492
1309	CGGCTTGCTGATGATTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAA	1368
493	ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys	512
1369	TCACTTCAGTGTACATGAGTACTACAATGCATCGAGGCGGAGGCGCGGAAGCACGTG	1428
513	ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluGluAlaValGluHisVal	532
1429	AAATGGCTGATAGCGGAGGTGTGGAAAGAAGATGATTCGGAGAGGGTGTTCGAAGGATTCT	1488
533	LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr---AlaIleAlaAlaGlyTyr	551

QY	1	ATGAGACGATCCGGAACACTACAAACCCCTTCTCGTTGGGATGTCAACTTCATCCAATCGCTT	60
		:::	
Db	54	IleArgArgSerGlyAsnTyrGlnProAlaLeuTyrAspSerAsnTyrIleGlnSerLeu	73
		:::	
QY	61	CTCAGTGACTATAAGGAGGACAAACACAGCTGATTAGGGCTTCTGAGCTGGTCACTTTGGTG	120
		:::	
Db	74	AsnThrProTyrThrGluGluArgHisLeuAspArgLysAlaGluLeuIleValGlnVal	93
		:::	
QY	121	AAGATGGAACCTGGAGAAAGAAACCGGATCAAATTCGACAACTTGAGTTGATCGATGACTTG	180
		:::	
Db	94	ArgIleLeuLeuLysGluLysMetGluProValGlnGlnLeuGluLeuIleHisAspLeu	113
		:::	
QY	181	CAGAGGATGGGGCTGTCGGATCATTTCCAAAATGAGTTCAAAAGAAATCTGTCTCTATA	240
		:::	
Db	114	LysTyrLeuGlyLeuSerAspPheGlnAspGluIleLysGluIleLeuGlyValIle	133
		:::	
QY	241	TATCTGCACCATCACTATTACAAGAACCCTTTTCCAAAAGAAAGAGGATCTCTACTCC	300
		:::	
Db	134	TyrAsnGluHisLysCysPheHisAsnAsn--GluValGluLysMetAspLeuTyrPhe	152
		:::	
QY	301	ACATCTCTTGCAATTTAGGCTCCTCAGAGAACATGGTTTTTCAAGTCGCACAAGAGGTATTC	360
		:::	
Db	153	ThrAlaLeuGlyPheArgLeuLeuArgGlnHisGlyPheAsnIleSerGlnAspValPhe	172
		:::	
QY	361	GATAGTTTCAAGAACGAGGAGGGT---GAGTTCAAAGAAAGCCCTTAGCGACGACACCAGA	417
		:::	

Db 513 ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluAlaValGluHisVal 532

QY 1429 AAATGGCTGATAGCGGAGGTGTGGAGAAGATGAATCGCGAGAGGGTGTCTGAAGGATCTT 1488

Db 533 LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr--AlaIleAlaAlaGlyTyr 551

QY 1489 CCATTCCGCAAGATTTTATAGGATGTGCAGTTGATTTAGGAGGATGGCGCAGTTGATG 1548

Db 552 ProPheProAspGlyMetValAlaGlyAlaAlaAsnIleGlyArgValAlaGlnPheIle 571

QY 1549 TACCATAATGAGATGGGCACGGCACACACCCCTATTATATACATCAACAAATGACCAGA 1608

Db 572 TyrLeuHisGlyAspGlyPheGlyValGlnHisSerLysThrTyrGluHisIleAlaGly 591

QY 1609 ACCTTATTCGAGCCCTTTGCA 1629

Db 592 LeuLeuPheGluProTyrAla 598

RESULT 13

US-09-900-797-26

; Sequence 26, Application US/09900797

; Publication No. US20030087406A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20030087406A11, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/900,797

; CURRENT FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: US/09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 598

; TYPE: PR

; ORGANISM: Salvia officinalis

US-09-900-797-26

Alignment Scores:

Pred. No.: 3.49e-128 Length: 598

Score: 1468.00 Matches: 281

Percent Similarity: 71.12% Conservative: 108

Best Local Similarity: 51.37% Mismatches: 152

Query Match: 50.48% Indels: 6

DB: 10 Gaps: 5

US-09-938-956-6 (1-1632) x US-09-900-797-26 (1-598)

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Db 54 IleArgArgSerGlyAsnTyrGlnProAlaLeuTrpAspSerAsnTyrIleGlnSerLeu 73

QY 61 CTCAGTGACTATAAGGAGGACAAACACGTCGATTAGGGCTTCTGAGCTGGTCACCTTGGTG 120

Db 74 AsnThrProTyrThrGluGluArgHisLeuAspArgLysAlaGluLeuIleValGlnVal 93

QY 121 AAGATGGAACCTGGAGAAAGAAACCGGATCAAATTCGACAACTTGAGTTGATCGATGACTTG 180

Db 94 ArgileLeuLeuLysGluLysMetGluProValGlnGlnLeuGluLeuIleHisAspLeu 113

QY 181 CAGAGGATGGGCTGTCCGATCATTTCCAAATGAGTTCAAAGAAATCTTGTCCCTCTATA 240

Db 114 LysTyrLeuGlyLeuSerAspPheGlnAspGluIleLysGluIleLeuGlyValIle 133

QY 241 TATCTCGACCATCACTATTACAAAGAACCCCTTTTCCAAAGAAAGGAGTCTCTACTCC 300

Db 134 TyrAsnGluHisLysCysPheHisAsnAsn---GluValGluLysMetAspLeuTyrPhe 152

QY 301 ACATCTCTTCGATTTAGGCTCCTCAGAGAACATGGTTTTCAGTCCGACAGAGGTATTC 360

Db 153 ThrAlaLeuGlyPheArgLeuLeuArgGlnHisGlyPheAsnIleSerGlnAspValPhe 172

QY 361 GATAGTTTCAACAACGAGGAGGT---GAGTTCAAAAGAAAGCCCTTAGCGACGACACCAGA 417

Db 173 AsnCysPheLysAsnGluLysGlyIleAspPheLysAlaSerLeuAlaGlnAspThrLys 192

QY 418 GGATTGTTGCAACTGTATGAAGCTTCCTTTCTGTTGACGGAAGGCGGAAACACCGCTCGAG 477

Db 193 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgLysGlyGluAspThrLeuGlu 212

QY 478 TCAGCGAGGGAATTCCGCCACCAATTTTGGAGGAAAAAGTGAACGAGGGTGGT----- 531

Db 213 LeuAlaArgGluPheAlaThrLysCysLeuGlnLysLysLeuAspGluGlyGlyAsnGlu 232

QY 532 GTTGATGGCGACCTTTTAAACAAGATCGCATATTCTTTGGACATCCCTCTTCATTGGAGG 591

Db 233 IleAspGluAsnLeuLeuTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg 252

QY 592 ATTAAGAGGCCAAATGCACCTGTGTGGATCGAATGGTATAGGAAGAGGCCCGACATGAAT 651

Db 253 IleGlnSerValGluAlaAlaArgTrpPheIleAspAlaTyrAlaArgProAspMetAsn 272

QY 652 CCAGTAGTGTGGAGCTTGCCATACTCGACTTAAATATTGTTCAAGCACAAATTTCAAGAA 711

Db 273 ProLeuIlePheGluLeuAlaLysLeuAsnPheAsnIleIleGlnAlaThrHisGlnGln 292

QY 712 GAGCTCAAAGAATCCTTCAGGTGGTGGAGAAAATACTGGGTTTGTGAGAAGCTGCCCTTC 771

Db 293 GluLeuLysAspLeuSerArgTrpTrpSerArgLeuCysPheProGluLysLeuProPhe 312

QY 772 GCAAGGGATAGACTGGTGAATGCTACTTTTGAATACTGGGATCATCGAGCCACGTCAG 831

Db 313 ValArgAspArgLeuValGluSerPhePheTrpAlaValGlyMetPheGluProHisGln 332

QY 832 CATGCAAGTCAAGGATAATGATGGGCAAAAGTCAACGCTCTGATTACGGTGATCGATGAT 891

Db 333 HisGlyTyrGlnArgLysMetAlaAlaThrIleIleValLeuAlaThrValIleAspAsp 352

QY 892 ATTTATGATGTCTATGGCACCTTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGAAGA 951

Db 353 IleTyrAspValTyrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg 372

QY 952 TGGGATATAAACTCAATCGACCAACTTCCCGATTACATGCAACTGTCTTCTTCGCACCTC 1011

Db 373 TrpAspThrGluSerIleThrArgLeuProTyrTyrMetGlnLeuCysTyrTrpGlyVal 392

QY 1012 AACAACTTCGTCGATGATACATCGTACGATGTTATGAAGGAGAAAGCGTCAACGTTATA 1071

Db 393 HisAsnTyrIleSerAspAlaAlaTyrAspIleLeuLysGluHisGlyPhePheCysLeu 412

QY 1072 CCCTACCTCGCGCAATCGTGGGTTGATTTCGGGATAAGTATATGTTAGAGGCACGGTGG 1131

Db 413 GlnTyrLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTrp 432

QY 1132 TTCTACGCGCGGCACAAACCAAGTTTGGAAAGAGTATTTTGGAGAACTCATGGCAGTCGATA 1191

Db 433 TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal 452

QY 1192 AGTGGGCCCTGTATGTTAAACGCACATATTCTTCCGAGTAACAGAT---TCGTTCCACAAAG 1248

Db 453 AlaSerProAlaIleIleSerProThrTyrPheThrPheAlaAsnAlaSerHisAspThr 472

QY 1249 GAGACCGTCGACAGTTTGTACAAATACCACGATTTAGTTCGTTGGTCATCCTTCGTTCTG 1308

Db 473 AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu 492

QY 1309 CGGCTTGTGATGATTTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAA 1368

Db 493 ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys 512


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QY 1369 TCACCTTCAGTGTACATGAGTGACTACAATGCATCGAGGCGGAGGCGGGAAGCAGGTG 1428
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QY 1429 AAATGGCTGATAGCGGAGGTGTGGAAGAAGATGAATGATCGGAGAGGGGTGTGCGAAGGATTCT 1488
Db 533 LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr--AlaIleAlaAlaGlyTyr 551
QY 1489 CCATTCCGGCAAGATTTTATAGGATGTGCAGTTGATTAGGAAGGATGGCGCAGTTGATG 1548
Db 552 ProPheProAspGlyMetValAlaGlyAlaAlaAsnIleGlyArgValAlaGlnPheIle 571
QY 1549 TACCATAATGGAGATGGCAGCGCACACACACCCCTATTATACATCAACAATGACCAGA 1608
Db 572 TyrLeuHisGlyAspGlyPheGlyValGlnHisSerLysThrTyrGluHisIleAlaGly 591
QY 1609 ACCTTATTCGAGCCCTTTGCA 1629
Db 592 LeuLeuPheGluProTyrAla 598

RESULT 14
US-09-887-586A-32
; Sequence 32, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-887-586A-32

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Alignment Scores:		
Pred. No.:	5.08e-69	556
Score:	836.00	182
Percent Similarity:	54.68%	116
Best Local Similarity:	33.39%	207
Query Match:	28.75%	40
DB:	9	10
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-938-956-6 (1-1632) x US-09-887-586A-32 (1-556)

QY	1	ATGAGACGATCCGGA	AACTACAACCCCTTCTCGTTGGGATGTCAACTTCATCCAATCGCTT	60
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Db	17	ValArgProIleAlaAsp	PheSerProSerLeuTrpGlyAspArgPheHisSerPheSer	36
QY	61	CTCAGTGACTATAAGG	AGGACAAACACGTCGATTAGGGCTTCTGAGCTGGTGCACCTTGGTG	120
		:::	:::	
Db	37	LeuAspAsnGlnIleAla	GlyLysTyr-----AlaGlnGluIleGluThrLeu---	52
QY	121	AAGATGGAACTGGAGA	GAAGAAACGGATCAAATT-----	153
			:::	
Db	53	-----	LysGluGlnSerArgIleLeuSerAlaSerSerArgArgThr	67
QY	154	-----CGACAAC	TTGAGTTGATCGATCTTGCCAGGAGGATGGGGCTGTCGATCATTTTC	207
		:::	:::	
Db	68	LeuAlaGluLysLeuAsp	LeuIleAspIleValGluArgLeuGlyIleAlaTyrHisPhe	87

QY	208	CAAAATGAGTTCAAAGAAATCTTTGCTCTATATAT-----CTCGACCAT	252
Db	88	GlulysGlnIleAspAspMetLeuAspGlnPheTyrLysAlaAspProAsnPheGluAla	107
QY	253	CACATATTACAAGAACCTTTTCCAAAAGAAAGGGATCTCTACTCCACATCTCTTGCA	312
Db	108	HisgluTyr-----AsnAspLeuGlnThrLeuSerValGln	119
QY	313	TTTAGGCTCCTCAGAGAACATGGTTTTTCAAGTCGCACAAGAGGTATTTCGATAGTTTCAAG	372
Db	120	PheArgLeuLeuArgGlnHisGlyTyrAsnIleSerProLysLeuPheIleArgPheGln	139
QY	373	AACGAGGAGGGTCAGTTCAAAGAAAGCCTTAGCGACGACACCAAGAGGATTGTTGCAACTG	432
Db	140	AspAlaLysGlyLysPheLysGluSerLeuCysAsnAspIleLysGlyLeuLeuAsnLeu	159
QY	433	TATGAAGCTTCCTTTCTGTTGACGGAAGCGGAAACCAACGCTCGAGTCAGCGAGGGAATTC	492
Db	160	TyrGluAlaSerHisValArgThrHisGlyGluAspIleLeuGluGluAlaLeuAlaPhe	179
QY	493	GCCACCAAATTTTGGAGGAAAAAGTGAACGAGGGTGGTGTGATGGCGACCTTTAAACA	552
Db	180	SerThrAlaHisLeuGluSerAlaAlaProHis-----LeuLysSerProLeuSerLys	197
QY	553	AGAAATCGCATATCTTTTGGACATCCCTCTTTCATTTGGAGGATTAAAGGCCAAATGCACCT	612
Db	198	GlnValThrHisAlaLeuGluGlnSerLeuHisLysSerIleProArgValGluThrArg	217
QY	613	GTGTGGATCGAATGGTATAGGAAGAGCGCCGACATGAATCCAGTAGTGTGGAGCTTGCC	672
Db	218	TyrPheIleSerIleTyrGluGluGluGluGlnLysAsnAspValLeuLeuGlnPheAla	237
QY	673	ATACTCGACTTAATATTGTTCAAGCACAAATTTCAAGAAGAGCTCAAAGAAATCCTTCAGG	732
Db	238	LysLeuAspPheAsnLeuLeuGlnMetLeuHisLysGlnGluLeuSerGluValSerArg	257
QY	733	TGGTGGAGAAATACTGGGTTTGTGAGAAAGCTGCCCTTCGCAAGGATAGACTGGTGGAA	792
Db	258	TrpTrpLysAspLeuAspPheValThrThrLeuProTyrAlaArgAspArgAlaValGlu	277
QY	793	TGCTACTTTTGGAAATACTGGGATCATCGAGCCAGCTCAGCATGCAAGTGCAAGGATAATG	852
Db	278	CysTyrPheTrpThrMetGlyValTyrAlaGluProGlnTyrSerGlnAlaArgValMet	297
QY	853	ATGGGCAAGTCAACGCTCTGATTACGGTGATCGATGATATTTATGATGTCTATGGCACC	912
Db	298	LeuAlaLysThrIleAlaMetIleSerIleValAspAspThrPheAspAlaTyrGlyIle	317
QY	913	TTAGAAGAACTCGAACAAATTCACCTGACCTCAATTCGAAGATGGGATATAAATCAATCGAC	972
Db	318	ValLysGluLeuGluIleTyrThrAspAlaIleGlnArgTrpAspIleSerGlnIleAsp	337
QY	973	CAACTTCCCGATTACATGCAACTGTGCTTTCTTGCACTCAACAACTTCGTCGATGATACA	1032
Db	338	ArgLeuProAspTyrMetLysIleSerTyrLysAlaLeuLeuAspLeuTyrAsnAspTyr	357
QY	1033	TCGTACGATGTTATGAAGGAGAAAGCGCTCAACGTTATACCTTACCTGCGGCAATCGTGG	1092
Db	358	GluMetGluLeuSerLysAspGlyArgSerAspValValHisTyrAlaLysGluArgMet	377
QY	1093	GTTGATTTGGCGGATAAGTATATGTTAGAGGCACGGTGGTTCCTACGGCGGGCACAACCA	1152
Db	378	LysGluIleValArgAsnTyrPheValGluAlaLysTrpPheIleGluGlyTyrMetPro	397
QY	1153	AGTTTGAAGAGTATTTGGAGAACTCATGGCAGTCGATAAGTGGCCCTGTATGTTAACG	1212
Db	398	ProValSerGluTyrLeuSerAsnAla---LeuAlaThrSerThrTyrTyrLeuLeuThr	416
QY	1213	CACATATTTCTCCGAGTAACAGATTTCGTTTCAAAAGGAGACCGTCGACAGTTTGTACAA	1272
Db	417	ThrThrSerTyrLeuGluMetLysSerAlaAsnLysGlnAspPheGluTrpLeuAlaLys	436

QY	1213	CACATATTCCTCCGAGTAACAGATTTCGTTTCAAAAGGAGACCGTCGACAGTTTGTGTACAAA	1272
Db	417	ThrThrSerTyrLeuGlyMetLysSerAlaAsnLysGlnAspPheGluTrpLeuAlaLys	436
QY	1273	TACCACGATTAGTTCGTTGGTGCATCCCTTCGTTCTGCGGCTTCGCTGATGATTTGGGAACC	1332
Db	437	AsnProLysIleLeuGluAlaAsnValThrLeuCysArgValIleAspIleAlaThr	456
QY	1333	TCGGTGAAGAGGTGAGCAGAGGGGATGTCCGAAATCATTCACTGCTACATGAGTGAC	1392
Db	457	TyrGluValGluLysGlyArgGlyGlnIleAlaThrGlyIleGluCysTyrMetArgAsp	476
QY	1393	TACAATGCATCGAGGGCGAGGGCGGGAAGCACGTGAAATGGCTGATAGCGGAGGTGTGG	1452
Db	477	TyrGlyValSerThrGluLysAlaMetGluLysPheGlnGluMetAlaGluThrAlaTrp	496
QY	1453	AAGAAGATGATCGCGAGAGGGGTGTCGAAGGATTCTCCATTCCGCAAGATTTTATAGGA	1512
Db	497	LysAspValAsn---GluGlyIleLeuArgProThrProValSerThrGluIleLeuThr	515
QY	1513	TGTGCAGTTGATTTAGGAAGGATGGCGCAGTTGTATGTAC---CATAAATGGAGATGGGCAC	1569
Db	516	ArgIleLeuAsnLeuAlaArgIleIleAspValThrTyrLysHisAsnGlnAspGlyTyr	535
QY	1570	GGCACACACACCCCT	1584
Db	536	-----ThrHisPro	538

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